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PROTEINS AND THEIR USES

Applicant(s): Zhu, et al.

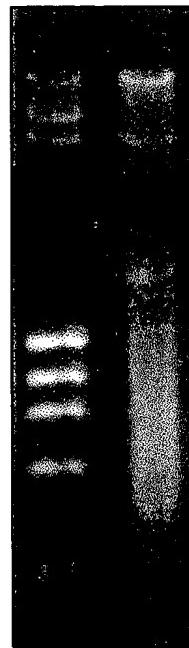
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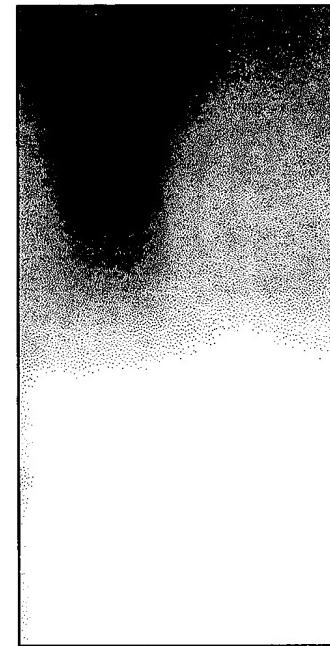
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M 1



1 2



**FIG. 1A**

**FIG. 1B**

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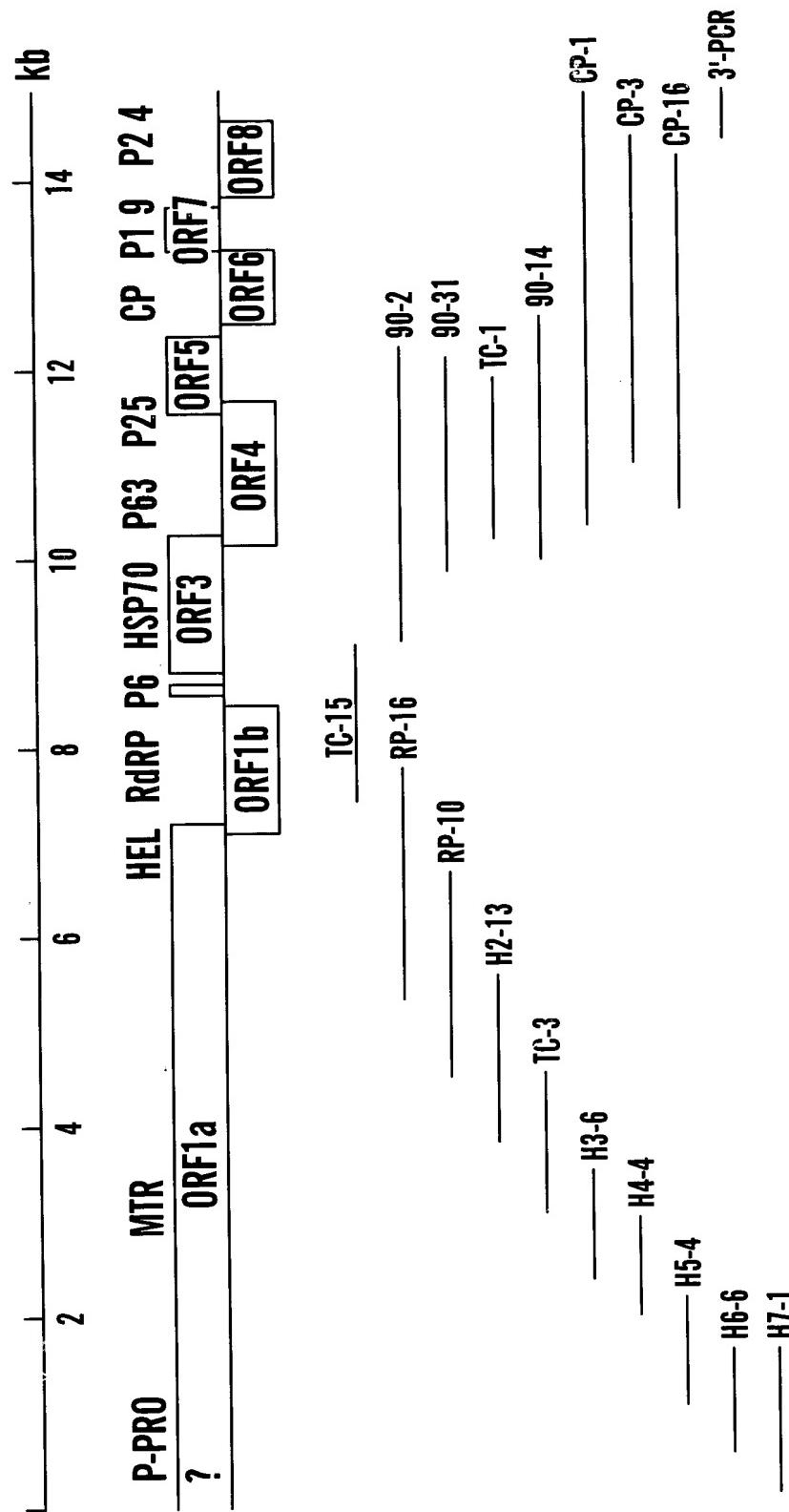


FIG. 2



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GLRaV2-PRO <sub>1</sub>	SRVIYPDGRCYLAHMRYLCAFYCRPFRESDYALGMWPTVARLACVEKNFGVEACGIALRGYYTSRNVYHCDYDSAYVKYFRNLSGRIG/G
GLRaV2-PRO <sub>2</sub>	TRIRYPNGPCYLAHCRYACAFILLRGFDPKRDPIDGAPTAAKLNRMVSELGERSLGLNLGYAYTSRGVFHCDYDAKFTKDLRLMSAVIA/G
BYV-P-PRO	LQYRPGEGLCYLAHAALCALQKRTFREEDPFGMPTKFVFAKLTKEKGPSALKHPVRGRQVSRLFHCDVASAFSSPFYSLPRFIG/G
Consensus	.....G.CYLAH....CA...R.F.....G..PT.....G.....G...SR...HCD.....I.G

## **FIG. 3A**

	MT I	MT IIa	MT II
GLRaV2-MTR	MSEATQNSLTRFPQPQELKFPHSHSSDHAAAASRLLENTELVRLCGNVSIDGGCPLFHLHSKTQRRVHVCRPVLDGKDAQRVVVRDLQ		
BYV-MTR	MGEAVQSGLTRAYPQFNLSPTHSVYSDHPAAAGSRLLENETLASMAKSSFDIGGCPLFHIK-RGSTDYHVCPIYDMKDAQRVVRSRELQ	MT III	
GLRaV2-MTR	YSNVRLG-DDDKILEGPRNIDICHYPLGACDHESAMMMVQVYDASLYEICGAMIKKSRTITYLTMVTGPFLDGRECVMESLDCEIEV		
BYV-MTR	ARGLVENLSREQLVEAQARVSVCPHTLGNCNVSDVLIMVQVYDASLNEIASAMVLKESKVAYLTMVTGPFLLEDEREAFALGCDVVV	MT IV	
GLRaV2-MTR	DVHADVVMYKFGSSCYSHKLSIIKDIMPYLTLLGGFLFSVEMYEVRMGVNYFKITKSEVSPSISCTKLLRYRANSDDVVVKVLPFD		
BYV-MTR	DTRRDMDVQYKFGSSCYCHKLSNIKSIMLTPAFTFSGNLFSVEMYENRMGVNYYKITRAYSPEIRGVKTLRYRACTEVVQVQLPFD		

## **FIG. 3B**

	HEL I	HEL II	HEL III	HEL IV
GLRaV2-Hel	FVFTNSSVDILLYEAPPGGKTTTLIDSFLKVFKKGEVSTMILTANKSSQVEILKKVEKEVSNIECQKRDKRSPKSIYTIDAYLMHHR			
BYV-Hel	FTFTNLSANVLLYEAPPGGKTTTLIKVFCETFSK--VNSLILTANKSREEILAKVNRIVLD-EGDTPLQTRDR--ILTIDSYLMNNR	HEL II		
GLRaV2-Hel	GCDADVLFIDECFCMVHAGSVLACIEFTRCHKVMIFGDSRQIHYIERNELDKCLYGDLDLRFVDLQCRVYGNISYRCPWDVCawlSTVYGNL		HEL III	
BYV-Hel	GLTCKVLYLDECFCMVHAGAAVACIEPTKCDSAILPGDSRQIRYGRCSLEDTAVLSDLNRFVDDESRVYGEVSYRCPWDVCawlSTFYPKT			HEL IV
GLRaV2-Hel	IATVKGESEGKSSMRINEINSVDDLVPDVGSTFLCMLQSEKLEISKHF--IRKGLTKLNVLTVHEAQGETYARVNLVRLKFQEDEPPKS			
BYV-Hel	VATTNLVSAGQSSMQVREIESVDDVEYSSEFYVLTMLQSEKKDLLKSGKRSRSSVEKPTVLTVHEAQGETYRKVNLVRTKFQEDDPFRS	HEL VI		
GLRaV2-Hel	IRHITVALSRHTDSLTYNVLAARRGDATCDAIQKAAELVNKFRVFPTSGGS			
BYV-Hel	ENHITVALSRHVESLTYSVLSSKRDDAIAQAIVKAKQLVDAYRVYPTSGGS	HEL V		

## **FIG. 3C**

	RdRP I	RdRP II	RdRP III
GLRaV2-RdRP	ICRFKLMVKRDAVKVLDSCLTKHSAAQNIMFHKRSINAIFSPIFNEVKNRIMCCLKPNIKPFTEMTNRDFASTVSNMLGDDDVYHIGEV		
BYV-RdRP	ITTFKLMVKRDAVKVLDSCLVKHPPAQNIMFHKAVNAIFSPCFDEFKNRVITCTNSNIVFFTEMNSTIASIAKEMLGSEHVNVEI	RdRP IV	
GLRaV2-RdRP	DFSKYDKSQDAFKAFEEVMYKELGVDEELLAIWMGERLSIANTLDGQLSFTIENQRKSGASNTWIGNSLVTLGILSLYYDVRNFEALY		RdRP V
BYV-RdRP	DFSKFDKSQLDAFIKSPERTLYSAFGFDEDLLDWQMGEYTSNATTLDGQLSFSVDNQRKSGASNTWIGNSIETLGILSMFYYTNRKFALF	RdRP VI	
GLRaV2-RdRP	ISGDDSLIFSRSEISNYADDICTDMGPETKFMSPSPVYFCSKFVVMCGHTFFFVDPYKLFWLGAVKEDVSMDFLFTFTSFKDLTSDF	RdRP VII	RdRP VIII
BYV-RdRP	VSGDDSLIFSESPIRNSADAMCTELGPETKFLTPSPVYFCSKFVMTGHDVFFVDPYKLLVKGASKDEVDEFLFEVFTSFKDLTKDL		
GLRaV2-RdRP	NDERLIQKLAELVALKYEVQTGNTTLAL		
BYV-RdRP	VDERVIELLTHLHVSKYGYESGDTYAAL		

## **FIG. 3D**



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GLRaV-2	CAUGAUAA <u>GG</u> CAG <u>GG</u> GU <u>UAG</u> CG <u>UAG</u> GU <u>UOGG</u> UC <u>GC</u> AG <u>GG</u> GA <u>UCCG</u> GU <u>JAGA</u>
BW	CA <u>CG</u> A <u>CCCG</u> C <u>AG</u> GG <u>GU</u> <u>UAG</u> C <u>TG</u> A <u>UOGC</u> U <u>CG</u> C <u>AGG</u> G <u>GA</u> <u>UCC</u> U <u>AAG</u> AGG
BYSV	CA <u>CG</u> A <u>UGA</u> A <u>AC</u> AG <u>GG</u> GU <u>UAG</u> CG <u>UAG</u> GU <u>UAGG</u> U <u>CG</u> C <u>AGG</u> CA <u>UCC</u> U <u>AAA</u> AGG
CTV	CA <u>CG</u> A <u>AC</u> GG <u>GU</u> <u>U<u>CG</u>GU</u> <u>UAG</u> GU <u>UAGG</u> U <u>AC</u> AC <u>AA</u> GU <u>UCC</u> U <u>UCC</u> U <u>CA</u> AGA
Consensus	CA.GA.....CG.GUU..GC....U....UC.CA.GC.AU.OC....AG.

## **FIG. 4A**

GLRaV-2	H D K Q R V <u>S</u> V V R S Q A I P R R
BW	H D P Q R V <u>S</u> S I R S Q A I P K R
BYSV	H D E Q R V <u>S</u> V V R S Q A I P K R
CTV	H E P A R V <u>G</u> V V R S Q A I P P R
Consensus	H . . . R V . . . R S Q A I P . R

## **FIG. 4B**



Title: GRAPEVINE LEAFROLL VIRUS TYPE 2,  
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FIG. 5



Title: GRAPEVINE LEAFROLL VIRUS (TYPE 2)

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FIG. 6A

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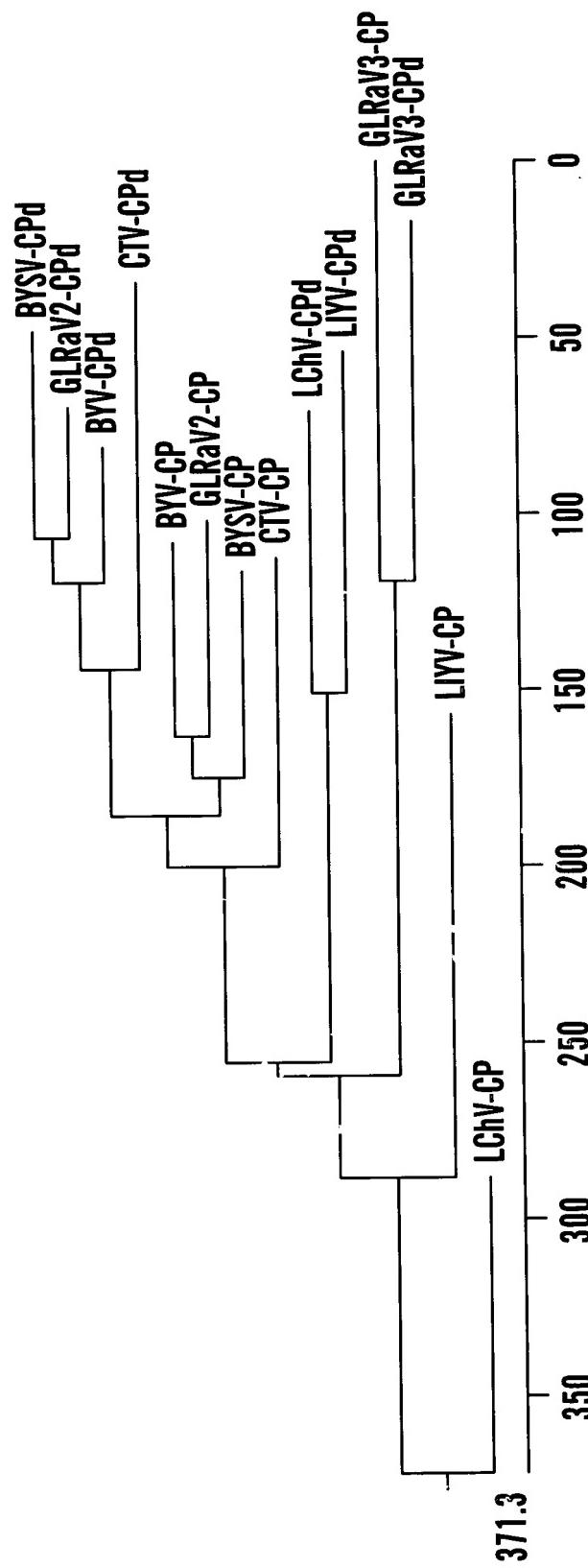


FIG. 6B

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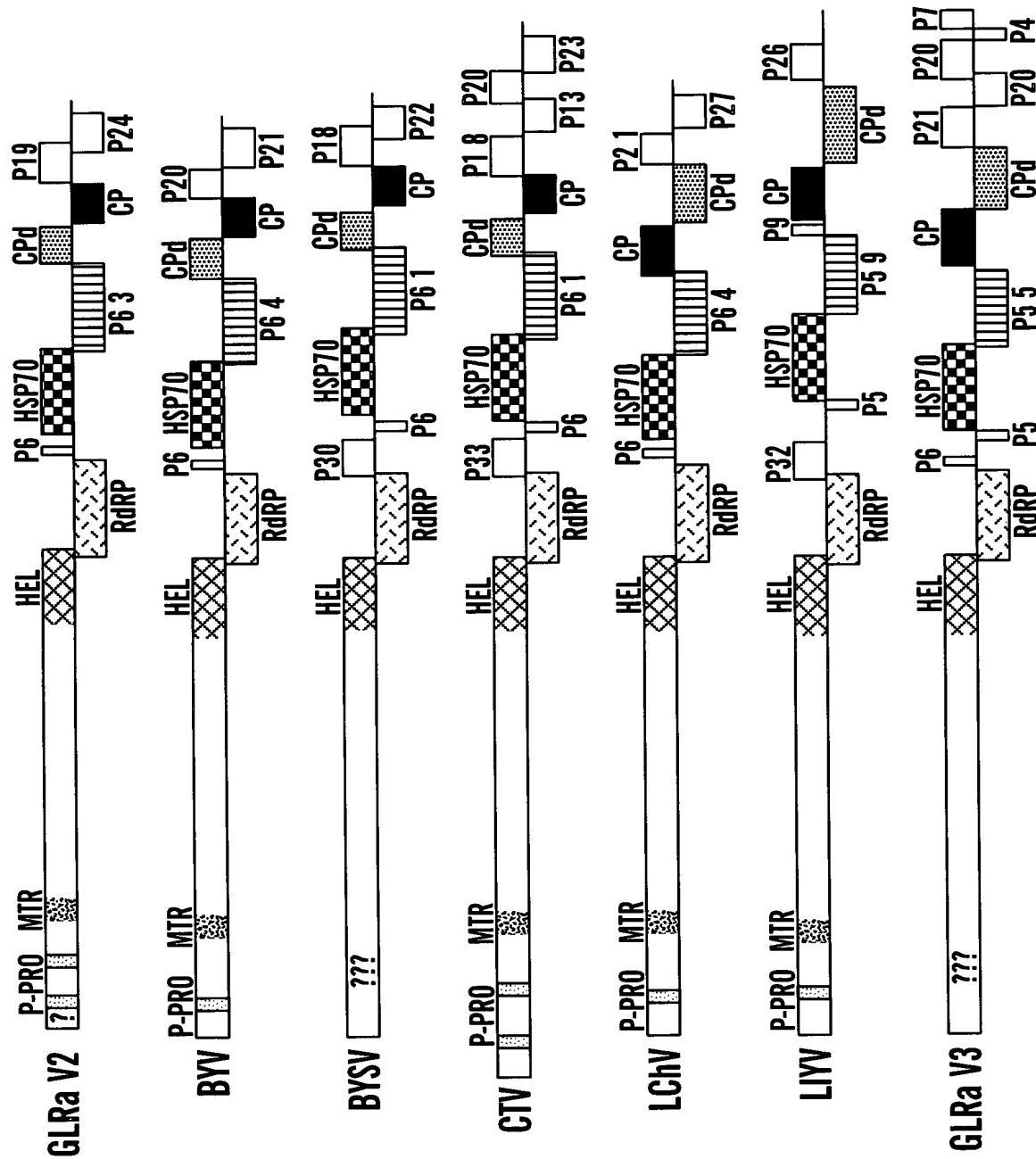


FIG. 7



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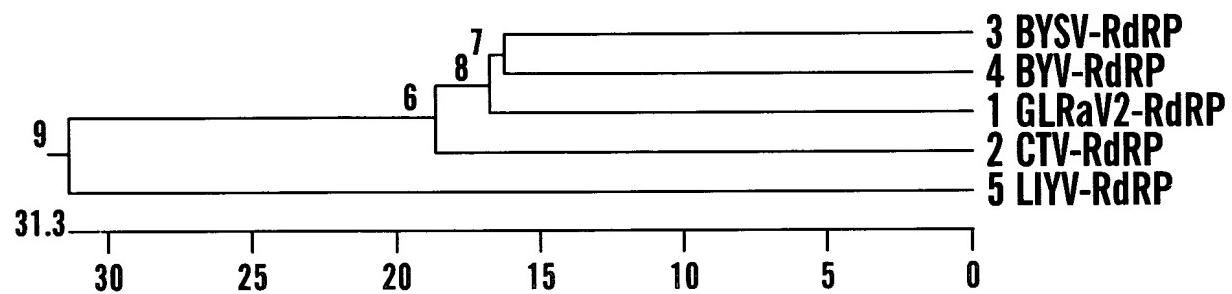
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**FIG. 8**

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**FIG. 9**

GLRaV2-Hsp90	MS-----NYSWESLFKKFYGEADWKYLSRSIAAHSSEIKTLDIRLYGGRVVKSEFESALP
BYV-HSP90	MTTRFSTPANYYWGELFRRFFGGQEWKNLMSEAASVRPRYSS--DFRFSDGVILSRKTFGESTG
BYSV-HSP90	MSRR-PTFAGYSWGSLSFKRHYGEPEWKSYLTEMKPKLSE--SITFYDGSSLTSAELRPARS
CTV-HSP90	MSSH-----HVVGSLSFRKYGEAIWKEYLSESTRNFDERNVL-DHTLSSGVVRRQSLNNAPQ
Consensus	M.....W..LF....G...WK.....G.....

GLRaV2-Hsp90	NSFEQE--LGLFILSEREVGWS-KLCGITVEEAAYDLTNPKAYKFTAETCSPDVKGEGQKYSMED
BYV-HSP90	ESFVREFSL-LLTFPKTYE--VCKLCGVAMELAINGMNRLSDYN-VSEFNIVDVKTVGCKFNIQS
BYSV-HSP90	GT--AEYEIALLIFSDSITKWSEKL-ERSIYRGLNQINNHISIYA-ETELEVTDVKTIGCKFTISA
CTV-HSP90	GTFENE--LALLYNSVVINDFVE-LTGMPPLKSLMTGIEDRKV---PDELI SVPDHEVGCRTLND
Consensus	.....E....L.....L.....E.....D....G.....

GLRaV2-Hsp90	VMNFMRLSNLDVNDKMLTEQCWSLSNSCGELINPDDKGRFVALTFKDRDTADDGAANVECRVGD
BYV-HSP90	VTEFVKKINGNVAEPSLVEHCWSLSNSCGELINPKDTKRFVSLIFKGKDIAESTDEAIVSSSYLD
BYSV-HSP90	VESFM---GGRASAAQVEHCWSLSNSCGELINPNNTARFIQLVFKDKAVTEQAQ-VNTSGSVSD
CTV-HSP90	VEVYLMRSRGEDFADLADEVHSWCLSNSCGRLLSSTEIDAYKTLVFT-KNF--DSNVSGVTTKLET
Consensus	V.....E..W..LSNSCG.L.....L.F.....

GLRaV2-Hsp90	YLVYAMSLFEQRTQKSQSGNISLYEKCEYIRTYLGSTDLFATPDRIPLLTGILYDFCKEYNVF
BYV-HSP90	YLSHCLNLYETCNLSSNSGKKSPLYDEFLKVIDYLENSLEYRSPSDNPLVAGILYDMCFEYNTL
BYSV-HSP90	YLVYCLQLYDNSKKKSAGRTQLMESYVSFIRDFFQHSDLYYRSPLDNPLLTGVLYDLCIEHNVL
CTV-HSP90	YLSYCISLYKKHCMKDD-DYFNLILPMFNCLMKVLASLGLFYEKHADNPLLTGMILEFCLENKVY
Consensus	YL.....L.....L.....L.....PL..G.L...

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GLRaV2-Hsp90	YSSYKRNVNDNFRFFLANYMPPLISDVFVFWQVVKPAPDV---RLLFELSAEELTLEVPTLSLIDSQ
BYV-HSP90	KSTYLNIESFDCFLSLYPLLSEVFMSNWERPAPDV---RLLFELDAEELLKVPITINMHDST
BYSV-HSP90	RGSYLNLDNFRFLKQTYLPMIDDIFDYSWELYAPDE---RLLFPIDPYEIKEVPTMSVIDAN
CTV-HSP90	YSTFKVNLDNVRFLFKSKVLPVVLTV---WDISEPPDPMDERVLIPFDPTDFVLDLPLKLNIDTM
Consensus	.....N.....F.....P.....W....PD.....R.L.....P....D..

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GLRaV2-Hsp90	VVVGHLRYVESYTSDPAIDALEDKLEAILKSSNPRSTAQLWVGFFCYGEFRTAQSRVVQRPG
BYV-HSP90	FLYKNKLRYLESYFEDDSNELIKVKVDSLTLRDNPTELKLAQRWVGFHCYGVFRTAQTRKVKRDA
BYSV-HSP90	VVLSNKLVYLDSYLENNSTLALEKKIISILCRDNEGIDEALWAFFCYGYRTARQRVVKRDP
CTV-HSP90	VVVGNIQRLLEYVVESDALDDLSQHVDLRLAADNPDLRVGLRWAGMFVYYGVYRCVVDRAYERPT
Consensus	.....L...N.....W.....YYG..R....R.V.R..

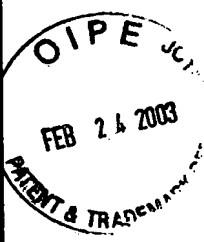
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GLRaV2-Hsp90	VYKTPDSV----GGFEINMKDVEKFFDKLQRELNPVSLRRQFNGARAHEAFKIFKNGNISFRP
BYV-HSP90	EYKLPPAL----GEFVINMSGVEEFFEEQKMKPSISVRRRCFGSLSHEAFSVFKRFGVGFPP
BYSV-HSP90	TYELDGIF----SKPIV-MSGVELFFDELQKRPVDVSLRRRFNGAKAGEAITVFKKLGISFPP
CTV-HSP90	LFRLPQKLLSQDDGESCSLHMGSVFNLVQVKVNDINVRQQFMGRHSEVALRLYRNGLRFPP
Consensus	.....M..VE..F...Q.....RR.F.G.....A.....F.P

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GLRaV2-Hsp90	ISRLNVPREFWYLNIDYFRHANRSGLTEEEILILNNISVDVRKLCAERACN----TLPSAKR
BYV-HSP90	ITRLNVPVKYSYLNVDYYRHVKRGLTQDELTILSNIEDVAEMCCEREVALQAR--RAQRGEKP
BYSV-HSP90	ITRLNAPSKEYSYLNIDYFKQANSGLTEPEKIILCNIAKDVDMMCAQRISSVKA----KP
CTV-HSP90	ISSVRLPAHHGYLYVDFYKRPDGAVTADELESIRQLRSSVDMCKDRVSITPPP FNRLRRGSSR
Consensus	I.....P.....YL..D.....T..E...L.....V...C..R.....

GLRaV2-Hsp90	FSKNHKSNIQSSRQERRIKDPLVVLKDLYEFQHKRAGWGSRSTRDLGSRADHAKGSG.
BYV-HSP90	FQGWGKTKNEISPHARSSIRVKKNNDSLNLWVKDVGARSQRRLNPLHR-----H
BYSV-HSP90	IAQRNG--EAINSACKTLPNTLVRALEKCLLNQAPSWNNTLTLNR
CTV-HSP90	TFRGRGARGASSRHMRSRDVATSGFNL PYHGRLY-----STS
Consensus	.....



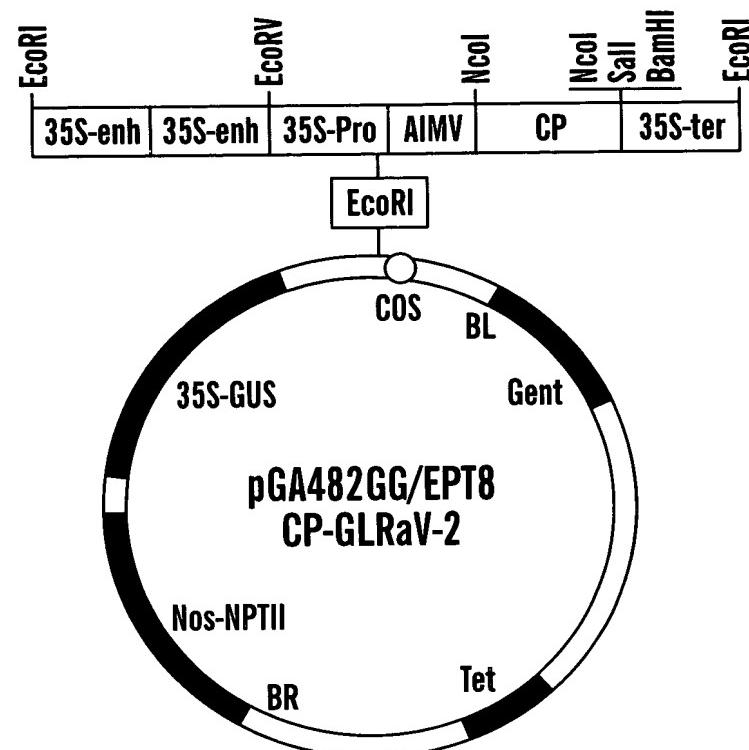
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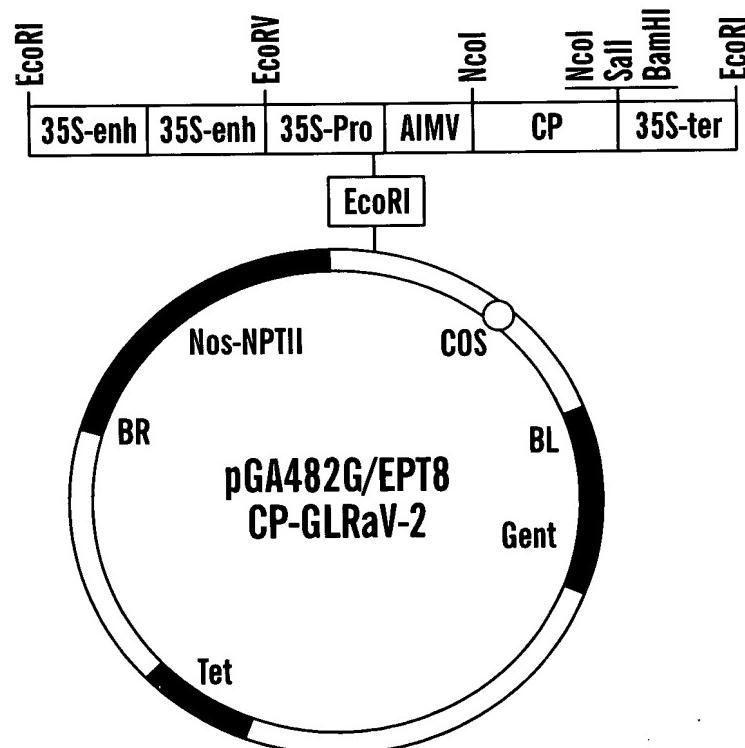
GLRaV2 3'-UTR	TTAAGCTTACTGACTTAATTAACCAACA <u>G</u> TGGTAAT <u>G</u> TGTGATGTGATGTTAGA	135
BYS 3'-UTR	TTAAGTCCTCACAGCTGACACGGCACC <u>A</u> G <u>C</u> GGTAGCTAGTGCGTAGTGAATTACGAA	95
BYSV 3'-UTR	TTAAGCCCTCACAGAGCGAGAAC <u>G</u> GT <u>C</u> GGCAAG <u>G</u> CCAA <u>T</u> AGTGTTAGTATAATTAA	181
CRV 3'-UTR	CTAAGCTCCCACAGAGTGGTAGGGCTCAAGTGAGCTTAACGTTAAGCTTAACTGAGGTGAAACCAAAGA	208
Consensus	.TAAG . . . AC . GAG . . . CAAG . G . . . T . . . A . . .	

**FIG. 10**

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**FIG. 11A**

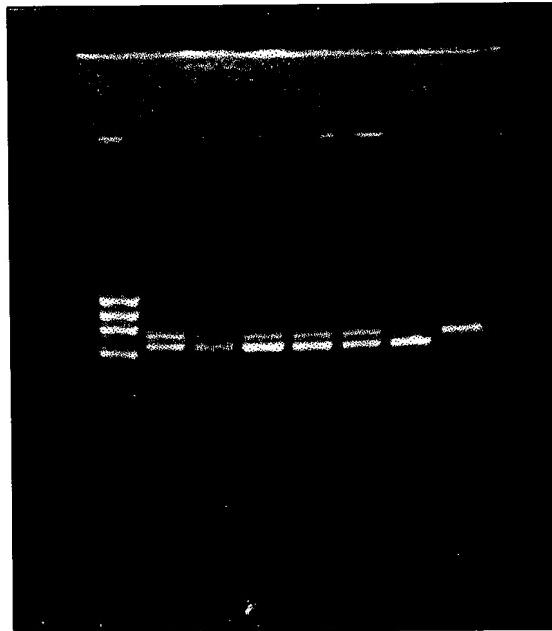


**FIG. 11B**

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**FIG. 12**

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**FIG. 13**



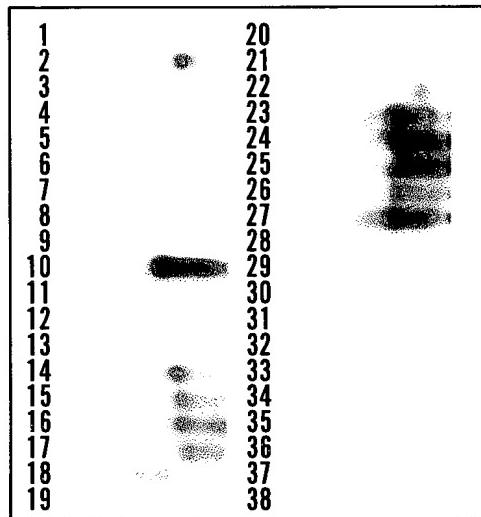
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***FIG. 14***